

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/532,014

Source: PT

Date Processed by STIC: 2/22/06

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 02/22/2006

PATENT APPLICATION: US/10/532,014

TIME: 08:26:00

Input Set : A:\Sequence-List.txt

Output Set: N:\CRF4\02222006\J532014.raw

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3 <110> APPLICANT: Karolinska Innovations AB
4     Ingelman-Sundberg, Magnus
5     Karlgren, Maria
6     Gomez, Alvin
8 <120> TITLE OF INVENTION: Drug target in cancer therapy
10 <130> FILE REFERENCE: P05980PC00/HAM/em
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/532,014
C--> 12 <141> CURRENT FILING DATE: 2005-04-20
12 <150> PRIOR APPLICATION NUMBER: SE0203137-5
13 <151> PRIOR FILING DATE: 2002-10-24
15 <150> PRIOR APPLICATION NUMBER: US 60/420,787
16 <151> PRIOR FILING DATE: 2002-10-24
18 <160> NUMBER OF SEQ ID NOS: 10
20 <170> SOFTWARE: PatentIn version 3.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 27
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <220> FEATURE:
W--> 28 <221> NAME/KEY: Primer
29 <222> LOCATION: (1)..(27)
30 <223> OTHER INFORMATION:
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34 gaggtggagg catcttcttc tcactctg                27
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38 <211> LENGTH: 25
39 <212> TYPE: DNA
40 <213> ORGANISM: Homo sapiens
42 <220> FEATURE:
W--> 43 <221> NAME/KEY: primer
44 <222> LOCATION: (1)..(25)
45 <223> OTHER INFORMATION:
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49 ctggatcagg gcgtccacat agctg                    25
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53 <211> LENGTH: 23
54 <212> TYPE: DNA
55 <213> ORGANISM: homo sapiens
57 <220> FEATURE:
W--> 58 <221> NAME/KEY: primer
59 <222> LOCATION: (1)..(23)
60 <223> OTHER INFORMATION:
W--> 63 <400> 3

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64 agctatgtgg acgccctgat cca                                23
67 <210> SEQ ID NO: 4
68 <211> LENGTH: 23
69 <212> TYPE: DNA
70 <213> ORGANISM: homo sapiens
72 <220> FEATURE:
W--> 73 <221> NAME/KEY: primer
74 <222> LOCATION: (1)..(23)
75 <223> OTHER INFORMATION:
W--> 78 <400> 4
79 acgcggtcta gctcctcctg cac                                23
82 <210> SEQ ID NO: 5
83 <211> LENGTH: 15
84 <212> TYPE: PRT
85 <213> ORGANISM: homo sapiens
87 <220> FEATURE:
88 <221> NAME/KEY: peptide
89 <222> LOCATION: (1)..(15)
90 <223> OTHER INFORMATION:
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95 Thr Met Arg Pro Arg Ala Gln Ala Leu Cys Ala Val Pro Arg Pro
96 1          5          10          15
99 <210> SEQ ID NO: 6
100 <211> LENGTH: 27
101 <212> TYPE: DNA
102 <213> ORGANISM: homo sapiens
104 <220> FEATURE:
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106 <222> LOCATION: (1)..(27)
107 <223> OTHER INFORMATION:
W--> 110 <400> 6
111 gacagatcta tggccctgct gctcttg                                27
114 <210> SEQ ID NO: 7
115 <211> LENGTH: 28
116 <212> TYPE: DNA
117 <213> ORGANISM: homo sapiens
119 <220> FEATURE:
W--> 120 <221> NAME/KEY: primer
121 <222> LOCATION: (1)..(28)
122 <223> OTHER INFORMATION:
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126 gactctagac tagggcctgg gcaccgca                                28
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130 <211> LENGTH: 490
131 <212> TYPE: PRT
132 <213> ORGANISM: homo sapiens
134 <400> SEQUENCE: 8
136 Met Ala Leu Leu Leu Leu Leu Phe Leu Gly Leu Leu Gly Leu Trp Gly
137 1          5          10          15

```

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140 Leu Leu Cys Ala Cys Ala Gln Asp Pro Ser Pro Ala Ala Arg Trp Pro
141      20      25      30
144 Pro Gly Pro Arg Pro Leu Pro Leu Val Gly Asn Leu His Leu Leu Arg
145      35      40      45
148 Leu Ser Gln Gln Asp Arg Ser Leu Met Glu Leu Ser Glu Arg Tyr Gly
149      50      55      60
152 Pro Val Phe Thr Val His Leu Gly Arg Gln Lys Thr Val Val Leu Thr
153 65      70      75      80
156 Gly Phe Glu Ala Val Lys Glu Ala Leu Ala Gly Pro Gly Gln Glu Leu
157      85      90      95
160 Ala Asp Arg Pro Pro Ile Ala Ile Phe Gln Leu Ile Gln Arg Gly Gly
161      100     105     110
164 Gly Ile Phe Phe Ser Ser Gly Ala Arg Trp Arg Ala Ala Arg Gln Phe
165      115     120     125
168 Thr Val Arg Ala Leu His Ser Leu Gly Val Gly Arg Glu Pro Val Ala
169      130     135     140
172 Asp Lys Ile Leu Gln Glu Leu Lys Cys Leu Ser Gly Gln Leu Asp Gly
173 145     150     155     160
176 Tyr Arg Gly Arg Pro Phe Pro Leu Ala Leu Leu Gly Trp Ala Pro Ser
177      165     170     175
180 Asn Ile Thr Phe Ala Leu Leu Phe Gly Arg Arg Phe Asp Tyr Arg Asp
181      180     185     190
184 Pro Val Phe Val Ser Leu Leu Gly Leu Ile Asp Glu Val Met Val Leu
185      195     200     205
188 Leu Gly Ser Pro Gly Leu Gln Leu Phe Asn Val Tyr Pro Trp Leu Gly
189      210     215     220
192 Ala Leu Leu Gln Leu His Arg Pro Val Leu Arg Lys Ile Glu Glu Val
193 225     230     235     240
196 Arg Ala Ile Leu Arg Thr Leu Leu Glu Ala Arg Arg Pro His Val Cys
197      245     250     255
200 Pro Gly Asp Pro Val Cys Ser Tyr Val Asp Ala Leu Ile Gln Gln Gly
201      260     265     270
204 Gln Gly Asp Asp Pro Glu Gly Leu Phe Ala Glu Ala Asn Ala Val Ala
205      275     280     285
208 Cys Thr Leu Asp Met Val Met Ala Gly Thr Glu Thr Thr Ser Ala Thr
209      290     295     300
212 Leu Gln Trp Ala Ala Leu Leu Met Gly Arg His Pro Asp Val Gln Gly
213 305     310     315     320
216 Arg Val Gln Glu Glu Leu Asp Arg Val Leu Gly Pro Gly Arg Thr Pro
217      325     330     335
220 Arg Leu Glu Asp Gln Gln Ala Leu Pro Tyr Thr Ser Ala Val Leu His
221      340     345     350
224 Glu Val Gln Arg Phe Ile Thr Leu Leu Pro His Val Pro Arg Cys Thr
225      355     360     365
228 Ala Ala Asp Thr Gln Leu Gly Gly Phe Leu Leu Pro Lys Gly Thr Pro
229      370     375     380
232 Val Ile Pro Leu Leu Thr Ser Val Leu Leu Asp Glu Thr Gln Trp Gln
233 385     390     395     400
236 Thr Pro Gly Gln Phe Asn Pro Gly His Phe Leu Asp Ala Asn Gly His

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237          405          410          415
240 Phe Val Lys Arg Glu Ala Phe Leu Pro Phe Ser Ala Gly Arg Arg Val
241          420          425          430
244 Cys Val Gly Glu Arg Leu Ala Arg Thr Glu Leu Phe Leu Leu Phe Ala
245          435          440          445
248 Gly Leu Leu Gln Arg Tyr Arg Leu Leu Pro Pro Pro Gly Val Ser Pro
249          450          455          460
252 Ala Ser Leu Asp Thr Thr Pro Ala Arg Ala Phe Thr Met Arg Pro Arg
253 465          470          475          480
256 Ala Gln Ala Leu Cys Ala Val Pro Arg Pro
257          485          490

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260 &lt;210&gt; SEQ ID NO: 9

261 &lt;211&gt; LENGTH: 2432

262 &lt;212&gt; TYPE: DNA

263 &lt;213&gt; ORGANISM: homo sapiens

265 &lt;220&gt; FEATURE:

266 &lt;221&gt; NAME/KEY: promoter

267 &lt;222&gt; LOCATION: (1)..(137)

268 &lt;223&gt; OTHER INFORMATION:

271 &lt;220&gt; FEATURE:

272 &lt;221&gt; NAME/KEY: exon

273 &lt;222&gt; LOCATION: (138)..(1608)

274 &lt;223&gt; OTHER INFORMATION:

W--&gt; 277 &lt;400&gt; 9

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278 gccctgcaaa ctgctcgttc cacattctcg ggggtggtggg gtgggtgggg tgcgggcacg      60
280 ccctcccgcg gaggcctata agggcgcggg ggggacgggg ccaggagggg gagtggagcc      120
282 tcaccagcca cgtcctc atg gcc ctg ctg ctc ttg ctg ttc ctg ggc ctc      170
283          Met Ala Leu Leu Leu Leu Leu Phe Leu Gly Leu
284          1          5          10
286 ctg ggg ctc tgg ggg ctg ctc tgc gcc tgc gcc caa gac ccc tcc cca      218
287 Leu Gly Leu Trp Gly Leu Leu Cys Ala Cys Ala Gln Asp Pro Ser Pro
288          15          20          25
290 gct gcc cgg tgg ccc ccg ggg cct cgc ccg ctg ccg ctc gtc ggg aac      266
291 Ala Ala Arg Trp Pro Pro Gly Pro Arg Pro Leu Pro Leu Val Gly Asn
292          30          35          40
294 ctg cac ttg ctg cgt ctg tgc caa cag gac cgg tcc ctg atg gag ctc      314
295 Leu His Leu Leu Arg Leu Ser Gln Gln Asp Arg Ser Leu Met Glu Leu
296          45          50          55
298 tca gaa cgc tac ggg ccg gtg ttc acc gtg cac ctg ggg cgc cag aag      362
299 Ser Glu Arg Tyr Gly Pro Val Phe Thr Val His Leu Gly Arg Gln Lys
300 60          65          70          75
302 acg gtg gtg ctg acg ggg ttc gag gcg gtc aaa gag gcg ctg gcg ggc      410
303 Thr Val Val Leu Thr Gly Phe Glu Ala Val Lys Glu Ala Leu Ala Gly
304          80          85          90
306 ccc ggg cag gag ctg gcc gac cgg cct ccc atc gcc atc ttc cag ctc      458
307 Pro Gly Gln Glu Leu Ala Asp Arg Pro Pro Ile Ala Ile Phe Gln Leu
308          95          100          105
310 atc cag cga ggt gga ggc atc ttc ttc tca tct ggg gcg cgc tgg agg      506
311 Ile Gln Arg Gly Gly Gly Ile Phe Phe Ser Ser Gly Ala Arg Trp Arg

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312	110	115	120	
314	gct gcc cgc cag ttc acg gtg cgt gcc ctg cac agc ctg ggc gtg ggc	554		
315	Ala Ala Arg Gln Phe Thr Val Arg Ala Leu His Ser Leu Gly Val Gly			
316	125 130 135			
318	cgg gag ccg gtg gct gac aag att ctg cag gag ctg aaa tgc ctc tct	602		
319	Arg Glu Pro Val Ala Asp Lys Ile Leu Gln Glu Leu Lys Cys Leu Ser			
320	140 145 150 155			
322	ggg cag ctg gat ggc tac aga ggc cgg ccc ttc ccg ctg gcc cta ctg	650		
323	Gly Gln Leu Asp Gly Tyr Arg Gly Arg Pro Phe Pro Leu Ala Leu Leu			
324	160 165 170			
326	ggc tgg gct ccc tcc aat atc acc ttc gcg ctc ctc ttc ggc cgc cga	698		
327	Gly Trp Ala Pro Ser Asn Ile Thr Phe Ala Leu Leu Phe Gly Arg Arg			
328	175 180 185			
330	ttt gac tac cgg gac ccc gtg ttt gtg tcc ctg ctg ggt ctc atc gat	746		
331	Phe Asp Tyr Arg Asp Pro Val Phe Val Ser Leu Leu Gly Leu Ile Asp			
332	190 195 200			
334	gag gtc atg gtc ctc ttg ggg tcc cct ggc ctg cag ctg ttc aac gtc	794		
335	Glu Val Met Val Leu Leu Gly Ser Pro Gly Leu Gln Leu Phe Asn Val			
336	205 210 215			
338	tac cca tgg ctc ggg gcc ctg ctc cag ctg cac cgg ccc gtc ctg cgc	842		
339	Tyr Pro Trp Leu Gly Ala Leu Leu Gln Leu His Arg Pro Val Leu Arg			
340	220 225 230 235			
342	aag atc gag gag gtc cgt gcc att ctg agg acc ctc ctg gag gcg cgg	890		
343	Lys Ile Glu Glu Val Arg Ala Ile Leu Arg Thr Leu Leu Glu Ala Arg			
344	240 245 250			
346	agg ccc cac gtg tgc ccg ggg gac ccc gtg tgc agc tat gtg gac gcc	938		
347	Arg Pro His Val Cys Pro Gly Asp Pro Val Cys Ser Tyr Val Asp Ala			
348	255 260 265			
350	ctg atc cag cag gga cag ggg gat gac ccc gag ggc ctg ttt gct gag	986		
351	Leu Ile Gln Gly Gln Gly Asp Pro Glu Gly Leu Phe Ala Glu			
352	270 275 280			
354	gcc aac gcg gtg gcc tgc acc ctg gac atg gtc atg gcc ggg acg gag	1034		
355	Ala Asn Ala Val Ala Cys Thr Leu Asp Met Val Met Ala Gly Thr Glu			
356	285 290 295			
358	acg acc tcg gcc acg ctg cag tgg gcc gca ctt ctg atg ggc cgg cac	1082		
359	Thr Thr Ser Ala Thr Leu Gln Trp Ala Ala Leu Leu Met Gly Arg His			
360	300 305 310 315			
362	ccg gac gtg cag ggc cgg gtg cag gag gag cta gac cgc gtg ctg ggc	1130		
363	Pro Asp Val Gln Gly Arg Val Gln Glu Glu Leu Asp Arg Val Leu Gly			
364	320 325 330			
366	cct ggg cgg act ccc cgg ctg gag gac cag cag gct ctg ccc tac aca	1178		
367	Pro Gly Arg Thr Pro Arg Leu Glu Asp Gln Gln Ala Leu Pro Tyr Thr			
368	335 340 345			
370	agc gcc gtg ctc cac gag gtg cag cgg ttc atc acg ctc ctg ccg cac	1226		
371	Ser Ala Val Leu His Glu Val Gln Arg Phe Ile Thr Leu Leu Pro His			
372	350 355 360			
374	gtg ccc cgc tgc acc gcg gcc gac aca cag ctg ggc ggc ttc ctg ctc	1274		
375	Val Pro Arg Cys Thr Ala Ala Asp Thr Gln Leu Gly Gly Phe Leu Leu			
376	365 370 375			

## VERIFICATION SUMMARY

DATE: 02/22/2006

PATENT APPLICATION: US/10/532,014

TIME: 08:26:01

Input Set : A:\Sequence-List.txt

Output Set: N:\CRF4\02222006\J532014.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:28 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1  
L:33 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:30  
L:43 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2  
L:48 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:45  
L:58 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3  
L:63 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:60  
L:73 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4  
L:78 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:75  
L:93 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:90  
L:105 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6  
L:110 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:107  
L:120 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7  
L:125 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:122  
L:277 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:268  
L:277 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:274